

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/005,318B

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1	Wrapped Nucleic <input type="checkbox"/> <input checked="" type="checkbox"/>	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3, as this will prevent "wrapping".	RECEIVED
2	Wrapped Aminos <input type="checkbox"/>	The amino acid number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3, as this will prevent "wrapping".	JUL 12 2000
3	Incorrect Line Length <input type="checkbox"/> <input checked="" type="checkbox"/>	The rules require that a line not exceed 72 characters in length. This includes spaces.	TECH CEN/NCI 1000/2900
4	Misaligned Amino Acid Numbering <input checked="" type="checkbox"/>	The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.	
5	Non-ASCII <input type="checkbox"/>	This file was not saved in ASCII (DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text so that it can be processed.	
6	Variable Length <input type="checkbox"/>	Sequence(s) _____ contain n's or Xaa's which represented more than one residue. As per the rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.	
7	PatentIn ver. 2.0 "bug" <input type="checkbox"/>	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence.	
8	Skipped Sequences (OLD RULES) <input type="checkbox"/>	Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS") (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: This sequence is intentionally skipped	
Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).			
9	Skipped Sequences (NEW RULES) <input type="checkbox"/>	Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence. <210> sequence id number <400> sequence id number 000	
10	Use of n's or Xaa's (NEW RULES) <input type="checkbox"/>	Use of n's and/or Xaa's have been detected in the Sequence Listing. Use of <220> to <223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.	
11	Use of <213>Organism (NEW RULES) <input type="checkbox"/>	Sequence(s) _____ are missing this mandatory field or its response.	
12	Use of <220>Feature (NEW RULES) <input type="checkbox"/>	Sequence(s) _____ are missing the <220>Feature and associated headings. Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown" Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)	
13	PatentIn ver. 2.0 "bug" <input type="checkbox"/>	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other means to copy file to floppy disk.	

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(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 286 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..282

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- (B) TYPE: nucleic acid
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(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..282

delete
duplicated
material

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GAT CAG AAG TGC AAG TGT GCT CGT ATT ACT TCT AGA ATC ATC CGT AGC
Asp Gln Lys Cys Lys Cys Ala Arg Ile Thr Ser Arg Ile Ile Arg Ser
15 20 25 30

48